complex; and bringing the complex thus formed into contact with a candidate compound;

or

(ii) incubating said first polypeptide with said second polypeptide in the presence of a candidate compound under conditions which would allow the first polypeptide to bind to the second polypeptide in the absence of the candidate compound;

and

(b) determining if said candidate compound inhibits or disrupts binding of the first polypeptide to the second polypeptide;

wherein said first polypeptide comprises a TRAM sequence consisting essentially of the sequence shown in SEQ ID NO:1 and said second polypeptide comprises a TRIM sequence which binds to a said TRAM sequence.

37. The method according to claim 36 wherein said candidate compound is a polypeptide comprising a TRAM and/or a TRIM sequence.

38. The method according to claim 36 wherein said first polypeptide and/or said second polypeptide is a viral polypeptide.

39. The method according to claim 38 wherein said viral polypeptide is a human papillomavirus (HPV) polypeptide.

40. The method according to claim 39 wherein said HPV polypeptide is E6.

41. The method according to claim 36 wherein said first polypeptide and/or said second polypeptide is a polypeptide found in eukaryotic cells.

42. The method according to claim 41 wherein said eukaryotic polypeptide is selected from transcription factors and cell cycle regulatory proteins.

43. The method according to claim 41 wherein said eukaryotic polypeptide is selected from mdm2, p53, TBP, E2F, YY1, CBP, p300, MyoD and TFIIB.

44. The method according to claim 36 wherein said TRIM sequence consists essentially of the sequence shown in SEQ ID NO:10.

45. A method for identifying a compound which interacts with a polypeptide comprising a TRAM sequence consisting essentially of the sequence shown in SEQ ID NO:1 and/or a TRIM sequence which binds to a said TRAM sequence, which method comprises:

(a) incubating a candidate compound with a polypeptide comprising a TRAM sequence and/or a TRIM sequence under suitable conditions; and

(b) determining if said candidate compound interacts with said polypeptide comprising a TRAM sequence and/or a TRIM sequence.

46. The method according to claim 45 wherein said compound is a polypeptide.

47. The method according to claim 45 wherein said TRIM sequence consists essentially of the sequence shown in SEQ ID NO:10.

48. A purified polypeptide consisting essentially of a TRAM sequence consisting essentially of the sequence shown in SEQ ID NO:1 or a TRIM sequence which binds to a said TRAM sequence.

49. A polynucleotide molecule comprising a coding region encoding the polypeptide according to claim 48.

50. The polynucleotide according to claim 49 further comprising an additional coding region linked to, and in frame with, the coding region encoding a said polypeptide.

51. The polynucleotide according to claim 49 in the form of a nucleic acid vector.

52. The method according to claim 36 wherein the TRAM sequence is selected from the group consisting of:

RKTNGGCPVCKQ (SEQ ID NO:3),

RKTNGGCPVCKQPI (SEQ ID NO:4), and

GCKRKTNGGCPVCKQLIAL (SEQ ID NO:5).

53. The method according to claim 36 wherein the first polypeptide is CBP.

54. The method according to claim 52 wherein the TRIM sequence is located within the second zinc finger of HPV-16 or -18 E6 protein.

55. The method according to claim 52 wherein the second polypeptide is HPV-16 E6 protein or HPV-18 E6 protein.

REMARKS

Favorable consideration of this application and entry of the foregoing amendments are requested.

New claims 36-55 are fully supported by an enabling disclosure, including the claims as originally filed.

A favorable Action on the merits is respectfully requested.